

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN  
AN 1974:504464 CAPLUS  
DN 81:104464  
TI Organic transition states. II. Methylenecyclopropane rearrangement.  
Two-step diradical pathway with a secondary minimum  
AU Hehre, W. J.; Salem, L.; Willcott, M. R.  
CS Lab. Chim. Theor., Univ. Paris-Sud, Orsay, Fr.  
SO Journal of the American Chemical Society (1974),  
96(13), 4328-30  
CODEN: JACSAT; ISSN: 0002-7863  
DT Journal  
LA English

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN  
AN 1974:505883 CAPLUS  
DN 81:105883  
TI Structure of coformycin, an unusual nucleoside of microbial origin  
AU Nakamura, Hikaru; Koyama, Gunji; Iitaka, Yoichi; Ohno, Masaji;  
Yagisawa, Naomasa; Kondo, Shinichi; Maeda, Kenji; Umezawa, Hamao  
CS Fac, Pharm. Sci., Univ. Tokyo, Tokyo, Japan  
SO Journal of the American Chemical Society (1974),  
96(13) 4327-8  
CODEN: JACSAT; ISSN: 0002-7863  
DT Journal  
LA English  
OS CASREACT 81:105883

# SEQ SEARCH SUMMARY

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 115 Seconds  
 (without alignments)  
 2330.181 Million cell updates/sec

Title: US-10-022-366A-2

Perfect score: 3949

Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	ABG70650	3949	100.0	747	5	EP 12/15587	Abg70650	Rabbit ad
2	Adj68732	3728	94.4	747	7	w0 03/87768	Adj68732	Human hea
3	Adm32868	3728	94.4	747	8	w0 04/24880	Adm32868	Protein s - human
4	Adq18475	3728	94.4	747	8	w0 04/48938	Adq18475	Human sof "
5	Adp87621	3728	94.4	747	8	w0 04/56961	Adp87621	Human NOV
6	Adp87625	3728	94.4	748	8	ADP87625 w0 04/56961	Adp87625	Human NOV
7	Adp87623	3728	94.4	751	8	ADP87623 "	Adp87623	Human NOV
8	Abg02232	3621.5	91.7	1813	4	w0 01/075067	Abg02232	Novel hum
9	Adp87685	3607	91.3	747	8	ADP87685	Adp87685	Rat AMP-a
10	Adp87635	3302	83.6	654	8	ADP87635	Adp87635	Human NOV
11	Adp87627	3302	83.6	654	8	ADP87627	Adp87627	Human NOV
12	Adp87637	3302	83.6	660	8	ADP87637	Adp87637	Human NOV
13	Adp87631	3302	83.6	660	8	ADP87631	Adp87631	Human NOV
14	Adp87629	3298	83.5	661	8	ADP87629	Adp87629	Human NOV
15	Adp87633	3298	83.5	661	8	ADP87633	Adp87633	Human NOV
16	Adm32870	2407.5	61.0	776	8	ADM32870	Adm32870	Protein s
17	Adb79947	2401	60.8	801	7	ADB79947	Adb79947	Rat AMP d
18	Adm05430	1917	48.5	438	7	ADM05430	Adm05430	Human pro

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 1444 Seconds  
(without alignments)  
184.773 Million cell updates/sec

Title: US-10-022-366A-2

Perfect score: 3949

Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result

Query

No.	Score	Match Length	DB	ID	Description
1	3949	100.0	747	15 US-10-022-366A-2	Sequence 2, Appli
2	3728	94.4	747	16 US-10-408-765A-538	Sequence 538, App
3	3613	91.5	752	16 US-10-322-281-772	Sequence 772, App
4	3511	88.9	732	16 US-10-322-281-769	Sequence 769, App
5	2401	60.8	801	14 US-10-205-219-187	Sequence 187, App
6	1917	48.5	438	15 US-10-108-260A-4115	Sequence 4115, Ap
7	1568	39.7	813	17 US-10-425-115-200019	Sequence 200019,
8	1490.5	37.7	544	16 US-10-437-963-171334	Sequence 171334,
9	1438	36.4	557	15 US-10-424-599-188513	Sequence 188513,
10	1096	27.8	577	17 US-10-425-115-328131	Sequence 328131,
11	1033.5	26.2	345	15 US-10-424-599-164796	Sequence 164796,
12	866.5	21.9	446	14 US-10-012-140-19	Sequence 19, Appl
13	710.5	18.0	268	17 US-10-425-115-328153	Sequence 328153,
14	615.5	15.6	219	16 US-10-767-701-35150	Sequence 35150, A
15	606.5	15.4	540	16 US-10-437-963-125822	Sequence 125822,
16	597	15.1	211	16 US-10-767-701-59704	Sequence 59704, A
17	549.5	13.9	308	15 US-10-424-599-276788	Sequence 276788,
18	416.5	10.5	145	16 US-10-437-963-140327	Sequence 140327,
19	348.5	8.8	241	16 US-10-767-701-34805	Sequence 34805, A
20	342	8.7	115	17 US-10-425-115-295726	Sequence 295726,
21	335	8.5	160	14 US-10-106-698-5825	Sequence 5825, Ap
22	324	8.2	65	9 US-09-864-761-42950	Sequence 42950, A
23	305	7.7	108	16 US-10-767-701-39882	Sequence 39882, A
24	291	7.4	106	16 US-10-767-701-41443	Sequence 41443, A
25	203	5.1	86	15 US-10-424-599-188512	Sequence 188512,
26	199	5.0	114	15 US-10-424-599-190598	Sequence 190598,
27	155	3.9	908	15 US-10-282-122A-47185	Sequence 47185, A
28	153.5	3.9	151	17 US-10-425-115-295117	Sequence 295117,
29	149	3.8	115	17 US-10-425-115-316899	Sequence 316899,
30	140	3.5	1116	14 US-10-369-493-2069	Sequence 2069, Ap
31	139	3.5	1102	14 US-10-369-493-1074	Sequence 1074, Ap
32	136.5	3.5	966	9 US-09-978-698-2	Sequence 2, Appli
33	135	3.4	968	14 US-10-342-224-14	Sequence 14, Appl
34	132	3.3	358	14 US-10-156-761-10132	Sequence 10132, A
35	130.5	3.3	1001	15 US-10-607-631-10	Sequence 10, Appl
36	127.5	3.2	1639	14 US-10-087-464-10	Sequence 10, Appl
37	126	3.2	699	15 US-10-282-122A-61334	Sequence 61334, A
38	126	3.2	961	16 US-10-767-701-47381	Sequence 47381, A
39	124	3.1	968	15 US-10-424-599-239683	Sequence 239683,
40	123	3.1	762	15 US-10-402-466A-20	Sequence 20, Appl
41	123	3.1	1019	16 US-10-408-765A-1661	Sequence 1661, Ap
42	122	3.1	965	14 US-10-150-559-2	Sequence 2, Appli
43	122	3.1	965	15 US-10-440-352-2	Sequence 2, Appli
44	122	3.1	972	15 US-10-282-122A-53353	Sequence 53353, A
45	120.5	3.1	2165	10 US-09-923-070A-29	Sequence 29, Appli

## ALIGNMENTS

### RESULT 1

US-10-022-366A-2

; Sequence 2, Application US/10022366A

; Publication No. US20040050316A1

; GENERAL INFORMATION:

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:30 ; Search time 43 Seconds  
(without alignments)  
1152.082 Million cell updates/sec

Title: US-10-022-366A-2

Perfect score: 3949

Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1724	43.7	600	4	US-09-270-767-32913	Sequence 32913, A
2	1724	43.7	600	4	US-09-270-767-48130	Sequence 48130, A
3	1461	37.0	610	4	US-09-248-796A-17399	Sequence 17399, A
4	1454	36.8	810	4	US-09-538-092-596	Sequence 596, App
5	140	3.5	226	4	US-09-270-767-42982	Sequence 42982, A
6	136.5	3.5	966	4	US-09-606-312-2	Sequence 2, Appli
7	132.5	3.4	334	4	US-09-543-681A-4632	Sequence 4632, Ap
8	127.5	3.2	338	4	US-09-489-039A-9479	Sequence 9479, Ap
9	124.5	3.2	352	4	US-09-328-352-6481	Sequence 6481, Ap
10	123	3.1	338	4	US-09-489-039A-8357	Sequence 8357, Ap
11	122	3.1	412	4	US-09-328-352-4751	Sequence 4751, Ap
12	120.5	3.1	2165	1	US-08-514-975B-2	Sequence 2, Appli

*Drosophila melanogaster*

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## OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 40 Seconds  
(without alignments)  
1796.848 Million cell updates/sec

Title: US-10-022-366A-2

Perfect score: 3949

Sequence: 1 MPLFKLPAEGKELEDDAMGSF . . . . . RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Maximum AACeN 1000 Listing first 45 summaries

Database : RTB 79:\*

Fix\_75:

1: piri:  
2: pir?;\*

2: pliz:  
3: pix3:\*

3: pins:  
4: pin4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9

Result	Query						
No.	Score	Match	Length	DB	ID		Description
1	3728	94.4	747	2	I39444	human	AMP deaminase (EC
2	3607	91.3	747	1	A27366	rat	AMP deaminase (EC
3	2407.5	61.0	776	2	S68146	human splice variant	AMP deaminase (EC
4	2406	60.9	774	2	S68147	"	AMP deaminase (EC
5	1888.5	47.8	760	2	A44313	"	AMP deaminase (EC
6	1727.5	43.7	865	2	T15771	C.elegans	hypothetical protein
7	1510	38.2	600	2	T01259		AMP deaminase homolog
8	1470.5	37.2	846	2	T39261		amp deaminase - fibroblast
9	1454	36.8	810	2	S49744		AMP deaminase (EC
10	1451	36.7	924	2	T50996		probable AMP deaminase
11	1390.5	35.2	605	2	S59996		AMP deaminase (EC)
12	671	17.0	797	2	S44546		probable membrane protein
13	656.5	16.6	888	2	S50801		AMP deaminase homolog
14	409.5	10.4	88	2	S50184		AMP deaminase (EC)

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 143 Seconds  
(without alignments)  
3005.628 Million cell updates/sec

Title: US-10-022-366A-2

Perfect score: 3949

Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	3728	94.4	747	1	AMD1_HUMAN	P23109 homo sapien
2	3607	91.3	747	1	AMD1_RAT	P10759 rattus norv
3	2788.5	70.6	717	2	Q6P3G5	Q6p3g5 brachydanio
4	2788.5	70.6	717	2	AAH63996	Aah63996 brachydan
5	2499	63.3	779	2	Q803X5	Q803x5 brachydanio
6	2422.5	61.3	766	2	Q8CFR4	Q8cfr4 mus musculu
7	2422.5	61.3	766	2	AAH56380	Aah56380 mus muscu
8	2412.5	61.1	766	1	AMD3_MOUSE	O08739 mus musculu
9	2406	60.9	767	1	AMD3_HUMAN	Q01432 homo sapien
10	2401	60.8	765	1	AMD3_RAT	O09178 rattus norv
11	1969	49.9	481	2	Q922J7	Q922j7 mus musculu
12	1890.5	47.9	798	2	Q9DBT5	Q9dbt5 mus musculu
13	1888.5	47.8	879	1	AMD2_HUMAN	Q01433 homo sapien
14	1830.5	46.4	860	2	Q7QFN2	Q7qfn2 anopheles g
15	1824.5	46.2	774	2	Q9VY76	Q9vy76 drosophila
16	1824.5	46.2	774	2	AAF48329	Aaf48329 drosophil